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RAW SEQUENCE LISTING

DATE: 07/02/2002

PATENT APPLICATION: US/10/007,706

TIME: 13:57:13

Input Set : A:\A70040-1.ST25.txt

Output Set: N:\CRF3\07022002\J007706.raw

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3 <110> APPLICANT: Penner, Reinhold
4     Fleig, Andrea
6 <120> TITLE OF INVENTION: METHODS OF SCREENING FOR LTRPC2 MODULATORS
8 <130> FILE REFERENCE: A-70040-1/RFT/NBC
10 <140> CURRENT APPLICATION NUMBER: US 10/007,706
11 <141> CURRENT FILING DATE: 2001-11-13
13 <150> PRIOR APPLICATION NUMBER: US 60/248,442
14 <151> PRIOR FILING DATE: 2000-11-13
16 <150> PRIOR APPLICATION NUMBER: US 60/254,528
17 <151> PRIOR FILING DATE: 2000-12-08
19 <160> NUMBER OF SEQ ID NOS: 10
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1503
25 <212> TYPE: PRT
26 <213> ORGANISM: Homo sapiens
28 <400> SEQUENCE: 1
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31 1             5             10             15
34 Phe Glu Gly Leu Pro Arg Arg Val Thr Asp Leu Gly Met Val Ser Asn
35             20             25             30
38 Leu Arg Arg Ser Asn Ser Ser Leu Phe Lys Ser Trp Arg Leu Gln Cys
39             35             40             45
42 Pro Phe Gly Asn Asn Asp Lys Gln Glu Ser Leu Ser Ser Trp Ile Pro
43             50             55             60
46 Glu Asn Ile Lys Lys Lys Glu Cys Val Tyr Phe Val Glu Ser Ser Lys
47 65             70             75             80
50 Leu Ser Asp Ala Gly Lys Val Val Cys Gln Cys Gly Tyr Thr His Glu
51             85             90             95
54 Gln His Leu Glu Glu Ala Thr Lys Pro His Thr Phe Gln Gly Thr Gln
55             100            105            110
58 Trp Asp Pro Lys Lys His Val Gln Glu Met Pro Thr Asp Ala Phe Gly
59             115            120            125
62 Asp Ile Val Phe Thr Gly Leu Ser Gln Lys Val Lys Lys Tyr Val Arg
63             130            135            140
66 Val Ser Gln Asp Thr Pro Ser Ser Val Ile Tyr His Leu Met Thr Gln
67 145            150            155            160
70 His Trp Gly Leu Asp Val Pro Asn Leu Leu Ile Ser Val Thr Gly Gly
71             165            170            175
74 Ala Lys Asn Phe Asn Met Lys Pro Arg Leu Lys Ser Ile Phe Arg Arg
75             180            185            190
78 Gly Leu Val Lys Val Ala Gln Thr Thr Gly Ala Trp Ile Thr Gly
79             195            200            205

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82 Gly Ser His Thr Gly Val Met Lys Gln Val Gly Glu Ala Val Arg Asp
83      210      215      220
86 Phe Ser Leu Ser Ser Ser Tyr Lys Glu Gly Glu Leu Ile Thr Ile Gly
87 225      230      235      240
90 Val Ala Thr Trp Gly Thr Val His Arg Arg Glu Gly Leu Ile His Pro
91      245      250      255
94 Thr Gly Ser Phe Pro Ala Glu Tyr Ile Leu Asp Glu Asp Gly Gln Gly
95      260      265      270
98 Asn Leu Thr Cys Leu Asp Ser Asn His Ser His Phe Ile Leu Val Asp
99      275      280      285
102 Asp Gly Thr His Gly Gln Tyr Gly Val Glu Ile Pro Leu Arg Thr Arg
103      290      295      300
106 Leu Glu Lys Phe Ile Ser Glu Gln Thr Lys Glu Arg Gly Gly Val Ala
107 305      310      315      320
110 Ile Lys Ile Pro Ile Val Cys Val Val Leu Glu Gly Gly Pro Gly Thr
111      325      330      335
114 Leu His Thr Ile Asp Asn Ala Thr Thr Asn Gly Thr Pro Cys Val Val
115      340      345      350
118 Val Glu Gly Ser Gly Arg Val Ala Asp Val Ile Ala Gln Val Ala Asn
119      355      360      365
122 Leu Pro Val Ser Asp Ile Thr Ile Ser Leu Ile Gln Gln Lys Leu Ser
123      370      375      380
126 Val Phe Phe Gln Glu Met Phe Glu Thr Phe Thr Glu Ser Arg Ile Val
127 385      390      395      400
130 Glu Trp Thr Lys Lys Ile Gln Asp Ile Val Arg Arg Arg Gln Leu Leu
131      405      410      415
134 Thr Val Phe Arg Glu Gly Lys Asp Gly Gln Gln Asp Val Asp Val Ala
135      420      425      430
138 Ile Leu Gln Ala Leu Leu Lys Ala Ser Arg Ser Gln Asp His Phe Gly
139      435      440      445
142 His Glu Asn Trp Asp His Gln Leu Lys Leu Ala Val Ala Trp Asn Arg
143      450      455      460
146 Val Asp Ile Ala Arg Ser Glu Ile Phe Met Asp Glu Trp Gln Trp Lys
147 465      470      475      480
150 Pro Ser Asp Leu His Pro Thr Met Thr Ala Ala Leu Ile Ser Asn Lys
151      485      490      495
154 Pro Glu Phe Val Lys Leu Phe Leu Glu Asn Gly Val Gln Leu Lys Glu
155      500      505      510
158 Phe Val Thr Trp Asp Thr Leu Leu Tyr Leu Tyr Glu Asn Leu Asp Pro
159      515      520      525
162 Ser Cys Leu Phe His Ser Lys Leu Gln Lys Val Leu Val Glu Asp Pro
163      530      535      540
166 Glu Arg Pro Ala Cys Ala Pro Ala Ala Pro Arg Leu Gln Met His His
167 545      550      555      560
170 Val Ala Gln Val Leu Arg Glu Leu Leu Gly Asp Phe Thr Gln Pro Leu
171      565      570      575
174 Tyr Pro Arg Pro Arg His Asn Asp Arg Leu Arg Leu Leu Pro Val
175      580      585      590
178 Pro His Val Lys Leu Asn Val Gln Gly Val Ser Leu Arg Ser Leu Tyr

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```

179          595          600          605
182 Lys Arg Ser Ser Gly His Val Thr Phe Thr Met Asp Pro Ile Arg Asp
183          610          615          620
186 Leu Leu Ile Trp Ala Ile Val Gln Asn Arg Arg Glu Leu Ala Gly Ile
187 625          630          635          640
190 Ile Trp Ala Gln Ser Gln Asp Cys Ile Ala Ala Ala Leu Ala Cys Ser
191          645          650          655
194 Lys Ile Leu Lys Glu Leu Ser Lys Glu Glu Glu Asp Thr Asp Ser Ser
195          660          665          670
198 Glu Glu Met Leu Ala Leu Ala Glu Glu Tyr Glu His Arg Ala Ile Gly
199          675          680          685
202 Val Phe Thr Glu Cys Tyr Arg Lys Asp Glu Glu Arg Ala Gln Lys Leu
203          690          695          700
206 Leu Thr Arg Val Ser Glu Ala Trp Gly Lys Thr Thr Cys Leu Gln Leu
207 705          710          715          720
210 Ala Leu Glu Ala Lys Asp Met Lys Phe Val Ser His Gly Gly Ile Gln
211          725          730          735
214 Ala Phe Leu Thr Lys Val Trp Trp Gly Gln Leu Ser Val Asp Asn Gly
215          740          745          750
218 Leu Trp Arg Val Thr Leu Cys Met Leu Ala Phe Pro Leu Leu Thr
219          755          760          765
222 Gly Leu Ile Ser Phe Arg Glu Lys Arg Leu Gln Asp Val Gly Thr Pro
223          770          775          780
226 Ala Ala Arg Ala Arg Ala Phe Phe Thr Ala Pro Val Val Val Phe His
227 785          790          795          800
230 Leu Asn Ile Leu Ser Tyr Phe Ala Phe Leu Cys Leu Phe Ala Tyr Val
231          805          810          815
234 Leu Met Val Asp Phe Gln Pro Val Pro Ser Trp Cys Glu Cys Ala Ile
235          820          825          830
238 Tyr Leu Trp Leu Phe Ser Leu Val Cys Glu Glu Met Arg Gln Leu Phe
239          835          840          845
242 Tyr Asp Pro Asp Glu Cys Gly Leu Met Lys Lys Ala Ala Leu Tyr Phe
243          850          855          860
246 Ser Asp Phe Trp Asn Lys Leu Asp Val Gly Ala Ile Leu Leu Phe Val
247 865          870          875          880
250 Ala Gly Leu Thr Cys Arg Leu Ile Pro Ala Thr Leu Tyr Pro Gly Arg
251          885          890          895
254 Val Ile Leu Ser Leu Asp Phe Ile Leu Phe Cys Leu Arg Leu Met His
255          900          905          910
258 Ile Phe Thr Ile Ser Lys Thr Leu Gly Pro Lys Ile Ile Ile Val Lys
259          915          920          925
262 Arg Met Met Lys Asp Val Phe Phe Phe Leu Phe Leu Leu Ala Val Trp
263          930          935          940
266 Val Val Ser Phe Gly Val Ala Lys Gln Ala Ile Leu Ile His Asn Glu
267 945          950          955          960
270 Arg Arg Val Asp Trp Leu Phe Arg Gly Ala Val Tyr His Ser Tyr Leu
271          965          970          975
274 Thr Ile Phe Gly Gln Ile Pro Gly Tyr Ile Asp Gly Val Asn Phe Asn
275          980          985          990

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```

278 Pro Glu His Cys Ser Pro Asn Gly Thr Asp Pro Tyr Lys Pro Lys Cys
279          995          1000          1005
282 Pro Glu Ser Asp Ala Thr Gln Gln Arg Pro Ala Phe Pro Glu Trp
283      1010          1015          1020
286 Leu Thr Val Leu Leu Leu Cys Leu Tyr Leu Leu Phe Thr Asn Ile
287      1025          1030          1035
290 Leu Leu Leu Asn Leu Leu Ile Ala Met Phe Asn Tyr Thr Phe Gln
291      1040          1045          1050
294 Gln Val Gln Glu His Thr Asp Gln Ile Trp Lys Phe Gln Arg His
295      1055          1060          1065
298 Asp Leu Ile Glu Glu Tyr His Gly Arg Pro Ala Ala Pro Pro Pro
299      1070          1075          1080
302 Phe Ile Leu Leu Ser His Leu Gln Leu Phe Ile Lys Arg Val Val
303      1085          1090          1095
306 Leu Lys Thr Pro Ala Lys Arg His Lys Gln Leu Lys Asn Lys Leu
307      1100          1105          1110
310 Glu Lys Asn Glu Glu Ala Ala Leu Leu Ser Trp Glu Ile Tyr Leu
311      1115          1120          1125
314 Lys Glu Asn Tyr Leu Gln Asn Arg Gln Phe Gln Gln Lys Gln Arg
315      1130          1135          1140
318 Pro Glu Gln Lys Ile Glu Asp Ile Ser Asn Lys Val Asp Ala Met
319      1145          1150          1155
322 Val Asp Leu Leu Asp Leu Asp Pro Leu Lys Arg Ser Gly Ser Met
323      1160          1165          1170
326 Glu Gln Arg Leu Ala Ser Leu Glu Glu Gln Val Ala Gln Thr Ala
327      1175          1180          1185
330 Arg Ala Leu His Trp Ile Val Arg Thr Leu Arg Ala Ser Gly Phe
331      1190          1195          1200
334 Ser Ser Glu Ala Asp Val Pro Thr Leu Ala Ser Gln Lys Ala Ala
335      1205          1210          1215
338 Glu Glu Pro Asp Ala Glu Pro Gly Gly Arg Lys Lys Thr Glu Glu
339      1220          1225          1230
342 Pro Gly Asp Ser Tyr His Val Asn Ala Arg His Leu Leu Tyr Pro
343      1235          1240          1245
346 Asn Cys Pro Val Thr Arg Phe Pro Val Pro Asn Glu Lys Val Pro
347      1250          1255          1260
350 Trp Glu Thr Glu Phe Leu Ile Tyr Asp Pro Pro Phe Tyr Thr Ala
351      1265          1270          1275
354 Glu Arg Lys Asp Ala Ala Ala Met Asp Pro Met Gly Asp Thr Leu
355      1280          1285          1290
358 Glu Pro Leu Ser Thr Ile Gln Tyr Asn Val Val Asp Gly Leu Arg
359      1295          1300          1305
362 Asp Arg Arg Ser Phe His Gly Pro Tyr Thr Val Gln Ala Gly Leu
363      1310          1315          1320
366 Pro Leu Asn Pro Met Gly Arg Thr Gly Leu Arg Gly Arg Gly Ser
367      1325          1330          1335
370 Leu Ser Cys Phe Gly Pro Asn His Thr Leu Tyr Pro Met Val Thr
371      1340          1345          1350
374 Arg Trp Arg Arg Asn Glu Asp Gly Ala Ile Cys Arg Lys Ser Ile

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375	1355	1360	1365
378	Lys Lys Met Leu Glu Val	Leu Val Val Lys Leu	Pro Leu Ser Glu
379	1370	1375	1380
382	His Trp Ala Leu Pro Gly	Gly Ser Arg Glu Pro	Gly Glu Met Leu
383	1385	1390	1395
386	Pro Arg Lys Leu Lys Arg	Ile Leu Arg Gln Glu	His Trp Pro Ser
387	1400	1405	1410
390	Phe Glu Asn Leu Leu Lys	Cys Gly Met Glu Val	Tyr Lys Gly Tyr
391	1415	1420	1425
394	Met Asp Asp Pro Arg Asn	Thr Asp Asn Ala Trp	Ile Glu Thr Val
395	1430	1435	1440
398	Ala Val Ser Val His Phe	Gln Asp Gln Asn Asp	Val Glu Leu Asn
399	1445	1450	1455
402	Arg Leu Asn Ser Asn Leu	His Ala Cys Asp Ser	Gly Ala Ser Ile
403	1460	1465	1470
406	Arg Trp Gln Val Val Asp	Arg Arg Ile Pro Leu	Tyr Ala Asn His
407	1475	1480	1485
410	Lys Thr Leu Leu Gln Lys	Ala Ala Ala Glu Phe	Gly Ala His Tyr
411	1490	1495	1500

414 <210> SEQ ID NO: 2
 415 <211> LENGTH: 4512
 416 <212> TYPE: DNA
 417 <213> ORGANISM: Homo sapiens
 419 <400> SEQUENCE: 2

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422	cccagaaggg	tactgacct	gggatgggc	tccaatctcc	ggcgagcaa	cagcagcctc	120
424	ttcaagagct	ggaggctaca	gtgccccttc	ggcaacaatg	acaagcaaga	aagcctcagt	180
426	tcgtggattc	ctgaaacat	caagaagaaa	gaatgcgtgt	atcttgtgga	aagttccaaa	240
428	ctgtctgatg	ctgggaaggt	ggtgtgtcag	tgtggctaca	cgcagagca	gcacttggag	300
430	gaggctacca	agccccacac	cttcaggggc	acacagtggt	acccaaagaa	acatgtccag	360
432	gagatgccaa	ccgatgcctt	tggcgacatc	gtcttcacgg	gcctgagcca	gaaggtgaaa	420
434	aagtacgtcc	gagtctccca	ggacacgccc	tccagcgtga	tctaccacct	catgaccag	480
436	cactgggggc	tggacgtccc	caatctcttg	atctcgggtg	ccgggggggc	caagaacttc	540
438	aacatgaagc	cgcggctgaa	gagcattttc	cgcagaggcc	tggtcaaggt	ggctcagacc	600
440	acaggggcct	ggatcatcac	aggggggtcc	cacaccggcg	tcatgaagca	ggtaggcgag	660
442	gcggtgcggg	acttcagcct	gagcagcagc	tacaaggaa	gcgagctcat	caccatcgga	720
444	gtcgcacact	ggggcactgt	ccaccgcgcg	gagggcctga	tccatcccac	gggcagcttc	780
446	cccgccgagt	acatactgga	tgaggatggc	caagggaacc	tgacctgcct	agacagcaac	840
448	cactctcact	tcctcctcgt	ggacgacggg	acccacggcc	agtacggggg	ggagattcct	900
450	ctgaggacca	ggctggagaa	gttcatatcg	gagcagacca	aggaaagagg	aggtgtggcc	960
452	atcaagatcc	ccatcgtgtg	cgtggtgctg	gagggcggcc	cgggcacggt	gcacaccatc	1020
454	gacaacgcc	ccaccaacgg	caccccctgt	gtggttgtgg	agggctcggg	ccgcgtggcc	1080
456	gacgtcattg	cccaggtggc	caacctgcct	gtctcggaca	tcactatctc	cctgatccag	1140
458	cagaaactga	gcgtgttctt	ccaggagatg	tttgagacct	tcacggaaa	caggattgtc	1200
460	gagtggacca	aaaagatcca	agatattgtc	cggaggcggc	agctgctgac	tgtcttccgg	1260
462	gaaggcaagg	atggtcagca	ggacgtggat	gtggccatct	tgcaggcctt	gctgaaagcc	1320
464	tcacggagcc	aagaccactt	tggccacgag	aactgggacc	accagctgaa	actggcagtg	1380
466	gcatggaatc	gcgtggacat	tgcccgcagt	gagatcttca	tggatgagtg	gcagtgggag	1440
468	ccttcagatc	tgcacccac	gatgacagct	gcactcatct	ccaacaagcc	tgagtttgtg	1500

VERIFICATION SUMMARY

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